



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140902

TO: Karen A Lacourciere
Location: REM-2D15/2C18
Art Unit: 1635
Wednesday, December 29, 2004
Case Serial Number: 08945805

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*
barbara.obryen@uspto.gov

Search Notes

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140902

STIC-Biotech/ChemLib

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 3:00 PM
To: STIC-Biotech/ChemLib
Subject: RE: Sequence search request 90/006175

Please search this using the CRF from 08945805

Thank-you!

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, December 20, 2004 2:52 PM
To: Lacourciere, Karen
Subject: RE: Sequence search request 90/006175

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you. Linda

-----Original Message-----

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 2:33 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 90/006175

Please search SEQ ID NO:1 for 90/006,175 in both the commercial databases and in the pending files
(interference)

Thank-you

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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SEQUENCE LISTING WARNING:

The sequence serial number you submitted was not listed in the CRF file. The attached search may not contain the exact sequence(s) listed under your serial number. The sequence listing used was in the CRF for an earlier serial number. The file wrapper of your case indicated it as a CIP, Divisional, Parent, Grandparent, Grandchild(ren) or Continuation of the earlier serial number.

Please remember that it is the examiner's responsibility to ensure that a case is in compliance with the sequence rules before allowing it.

*CRF from 08-945805 (US 6026203
used for this search)*

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GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

nucleic - nucleic search, using **Sw** model

on: December 28, 2004, 07:31:07 ; search time 1772 Seconds
 sequence: 1 ccttgaaggattccctcc 20
 scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

searched: 4526729 seqs, 23644889745 residues

total number of hits satisfying chosen parameters: 9053458

DB seq length: 0
 maximum DB seq length: 2000000000
 hit-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

database : GenEmbl_*

1: gb_ba:/*
 2: gb_hhg:/*
 3: gb_in:/*
 4: gb_cm:/*
 5: gb_ov:/*
 6: gb_pat:/*
 7: gb_bp:/*
 8: gb_pl:/*
 9: gb_pr:/*
 10: gb_ro:/*
 11: gb_se:/*
 12: gb_sy:/*
 13: gb_un:/*
 14: gb_y1:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

built	No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	20	6	BD222318			BD222318 Method f
2	20	100.0	20	6	AX937169			AX937169 Sequence
3	20	100.0	20	6	BD16242			BD16242 Pharmace
4	20	100.0	20	6	BD173898			BD173898 Pharmace
5	20	100.0	36	6	AR211932			AR211932 Sequence
6	20	100.0	36	6	AR41437			AR41437 Sequence
7	20	100.0	46	6	AR211931			AR211931 Sequence
8	20	100.0	46	6	AR41436			AR41436 Sequence
9	20	100.0	130	6	AX824437			AX824437 Sequence
10	20	100.0	397	11	G73338			G73338 SGV-R233
11	20	100.0	411	11	G73796			G73796 SGV-R137
12	20	100.0	604	10	G71795			G71795 SCV-R136
13	20	100.0	992	10	MMYCAM1B1			U12878 Mus muscu
14	20	100.0	1032	6	ARI174653			ARI174653 Sequence
15	20	100.0	1032	6	BD140422			BD140422 Endothel
16	20	100.0	2321	10	MMYCAM01			I22301 Mus muscu
17	20	100.0	2355	9	S50587			S50587 VCAm1=vasc
18	20	100.0	2396	9	HUMVACA			T142327 Mus muscu
19	20	100.0	2458	10	MMYCAM1			T142327 Human vasc

ALIGNMENTS

10	20	100	0	2501	6	CQ778548	Sequence
11	20	100	0	3418	10	BC029823	Mus muscu
12	20	100	0	3691	6	AX188354	Sequence
13	20	100	0	5607	9	HM0VCA01A	M73255 Human -vscu
14	20	100	0	22658	9	AF336818	Homo sapi
15	20	100	0	152558	9	AC033428	Homo sapi
16	20	100	0	194552	10	AC108909	Mus muscu
17	20	100	0	22871	2	AC122888	Mus muscu
18	20	100	0	268180	2	AC113762	Fattus no
19	20	100	0	287919	2	AC109094	Fattus no
0	18	92	0	110000	1	AE017180	Continuation (16 o
1	18	90	0	19	6	AR211934	Sequence
2	18	90	0	19	6	AR191439	Sequence
3	18	90	0	160765	2	AC136005	Homo sapi
4	18	90	0	161027	9	AC136006	Homo sapi
5	18	90	0	169073	8	AC132491	Orzya sat
6	18	90	0	179559	2	AC112930	Mus muscu
7	18	90	0	213073	9	AC092653	Homo sapi
8	17	87	0	63	6	AXB4455	Sequence
9	17	87	0	63	6	AXB24456	Sequence
10	17	87	0	1360	14	AY486462	Hyposoter
11	17	87	0	90554	9	AP001124	Homo sapi
12	17	87	0	166560	10	AC115924	AC115924 Mus muscu
13	17	87	0	179080	2	AC092514	Dapiro anu
14	17	87	0	203822	2	AC146825	Octolemar
15	17	87	0	219796	2	AC146734	Otolemar

FEATURES	Source	PC	G01N33/15//C12N5/10,C12N5/00
		CC	Primer Against Human NF-kB
		CC	PCR Primer Against Human NF-kB
		FH	Key
		FT	Source
		FT	Location/Qualifiers
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			1..20 Location/Qualifiers
			1..20 /organism="Homo sapiens"
			/mol_type="genomic DNA"
			/db_xref=taxon:9606"

SUMMARIES

SUMMARIES							DESCRIPTIONS							
built No.	Score	Query Match	Length	DB ID	Method	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
1	20	100	0	20	6	BD272318	BD272318	AX937169	AX937169	BD166242	BD173898	AR211932	AR491437	AR211931
2	20	100	0	20	6	AX937169	Sequence	BD166242	Pharmaceu	BD173898	AR211932	AR491437	Sequence	AR211931
3	20	100	0	20	6	BD166242	Sequence	BD173898	Pharmaceu	AR211932	Sequence	AR491437	Sequence	AR211931
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5	20	100	0	36	6	AR491437	Sequence	AR211931	Sequence	AR211931	Sequence	AR211931	Sequence	AR211931
6	20	100	0	36	6	AR491437	Sequence	AR211931	Sequence	AR211931	Sequence	AR211931	Sequence	AR211931
7	20	100	0	46	6	AR211931	Sequence	AR491436	Sequence	AX824437	Sequence	G73338	SGV-R33	G73795
8	20	100	0	46	6	AR491436	Sequence	AX824437	Sequence	G73338	SGV-R33	G73796	SGV-R33	G73795
9	20	100	0	130	6	AX824437	Sequence	G73338	SGV-R33	G73796	SGV-R33	G73795	SGV-R33	G73795
10	20	100	0	397	11	G73338	Sequence	G73796	SGV-R33	G73796	SGV-R33	G73795	SGV-R33	G73795
11	20	100	0	411	11	G73796	Sequence	G73796	SGV-R33	G73796	SGV-R33	G73795	SGV-R33	G73795
12	20	100	0	604	11	G73795	Sequence	G73795	SGV-R33	G73795	SGV-R33	G73795	SGV-R33	G73795
13	20	100	0	992	10	MMVCA1B1	MMVCA1B1	U12478	Mus musculu	U12478	Mus musculu	U12478	Mus musculu	U12478
14	20	100	0	1032	6	AR174653	Sequence	AR174653	Sequence	BD140422	Sequence	BD140422	Sequence	BD140422
15	20	100	0	1032	6	BD140422	Sequence	BD140422	Endotheli	L22301	Mus musculu	L22301	Mus musculu	L22301
16	20	100	0	2321	10	MUSVCA1	MUSVCA1	S50587	VCA1=vascu	S50587	VCA1=vascu	S50587	VCA1=vascu	S50587
17	20	100	0	2355	9	S50587	Sequence	U12431	Human_vascu	U12431	Human_vascu	U12431	Human_vascu	U12431
18	20	100	0	2396	9	HUMVCA1A	HUMVCA1A	U12431	Mus musculu	U12431	Mus musculu	U12431	Mus musculu	U12431
19	20	100	0	2458	10	MMVCA127	MMVCA127	U12431	Mus musculu	U12431	Mus musculu	U12431	Mus musculu	U12431

1. .20
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 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 2
 AX937169 AX937169 20 bp DNA linear PAT 06-JAN-2004
 LOCUS Sequence 9 from Patent WO03091432.
 DEFINITION
 ACCESSION BD173898
 VERSION 4
 KEYWORDS
 SOURCE
 ORGANISM synthetic construct
 REFERENCE 1. Lee, I.-K. and Morishita, R.
 AUTHORS
 TITLE Circular dumbbell decoy oligodeoxynucleotides (cdodn) containing
 dna binding sites of transcription factors
 JOURNAL Patent: WO 03091432-A 1 06-NOV-2003;
 FEATURES
 SOURCE Anges MG, Inc. (JP) ; Lee, In-kyu (KR)
 Location/Qualifiers 1. .20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32650"
 /note="Description of Artificial Sequence: NF-?B decoy"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 3
 BD166242 BD166242 20 bp DNA linear PAT 17-JAN-2003
 LOCUS Pharmaceutical composition containing decoy and utilization
 DEFINITION thereof
 ACCESSION BD166242
 VERSION 1
 KEYWORDS
 SOURCE
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 20) Morishita, R., Aoki, M., Ogiwara, T. and Kawasaki, T.
 AUTHORS
 TITLE Pharmaceutical composition containing decoy and utilization thereof
 JOURNAL Patent: JP 2002193813-A 1 10-JUL-2002;
 FEATURES
 SOURCE
 ORGANISM
 COMMENT OS Artificial Sequence
 PN JP 2002193813-A/1
 PD 10-JUL-2002
 PF 27-DEC-2002 JP 2000399613
 PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIRO OGIVARA, TOMIO KAWASAKI
 PC A61K31/7088, A61K47/46, A61P9/00, A61P9/10, A61P11/06, A61P13/12,
 PC A61P17/00,
 PC A61P29/00, A61B35/00, C12N15/09, C12N15/00
 CC Description of Artificial Sequence: NF-kappaB decoy FH
 KEY
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 /organism="Artificial Sequence".
 FT Location/Qualifiers

FEATURES

1. .20
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 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 4
 BD173898 BD173898 20 bp DNA linear PAT 18-FEB-2003
 LOCUS BD173898
 DEFINITION Pharmaceutical compositions containing decoy and method of using
 the same.
 ACCESSION BD173898
 VERSION GI:28815231
 WO 02066070-A/1.
 KEYWORDS synthetic construct
 SOURCE
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 20) Morishita, R., Aoki, M., Ogiwara, T., Kaneda, Y. and Nakamura, H.
 AUTHORS
 TITLE Pharmaceutical compositions containing decoy and method of using
 the same
 JOURNAL Patent: WO 02066070-A 1 29-AUG-2002;
 ANGES MG INC, RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIRO OGIVARA,
 YASUFUMI KANEDA, HIROSHIGE NAKAMURA
 COMMENT OS Artificial Sequence
 PN WO 02066070-A/1
 PD 29-AUG-2002
 PF 06-FEB-2002
 PR 20-FEB-2001 JP 01P 04350
 PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIRO OGIVARA, YASUFUMI
 KANEDA,
 PI HIROSHIGE NAKAMURA
 PC A61K48/00, A61K31/711, A61K9/06, A61K47/10, A61P17/00,
 PC A61P17/04
 CC Description of Artificial Sequence: NF-kappaB decoy FH
 KEY
 FT Source 1. .20
 /organism="Artificial Sequence".
 FT Location/Qualifiers

1. .20
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:2630"

ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 5
 AR211932 AR211932 36 bp DNA linear PAT 20-JUN-2002
 LOCUS AR211932
 DEFINITION Sequence 2 from patent US 6399376.
 ACCESSION AR211932
 VERSION AR211932.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 36)
 AUTHORS Medford, R.M. and Bennett, C. Frank.
 TITLE Modulation of vascular cell adhesive molecule expression through
 oligonucleotide interactions
 JOURNAL Patent: US 6399376-A 2 JUN-2002;
 FEATURES Location/Qualifiers
 SOURCE 1 .36
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 16 CCTTGAGGGATTCCCTCC 35

RESULT 6
 LOCUS AR491437
 DEFINITION Sequence 2 from patent US 6713621. 36 bp DNA
 ACCESSION AR491437
 VERSION GI:47259436
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Medford, R.M. and Bennett, C.F.
 TITLE Chimeric Oligonucleotides for modulating gene expression
 JOURNAL Patent: US 6713621-A 230-MAR-2004;
 FEATURES Location/Qualifiers
 SOURCE 1 .36
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 21 CCTTGAGGGATTCCCTCC 40

RESULT 8
 LOCUS AR491436
 DEFINITION Sequence 1 from patent US 6713621. 46 bp DNA
 ACCESSION AR491436
 VERSION GI:47259435
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 46)
 AUTHORS Medford, R.M. and Bennett, C.F.
 TITLE Chimeric oligonucleotides for modulating gene expression
 JOURNAL Patent: US 6713621-A 30-MAR-2004;
 FEATURES Location/Qualifiers B

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 21 CCTTGAGGGATTCCCTCC 40

RESULT 9
 LOCUS AX824437
 DEFINITION Sequence 16 from Patent WO03071281. 130 bp DNA
 ACCESSION AX824437
 VERSION AX824437.1 GI:39750436
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Boersma, C.J. and van Gool, A.J.
 TITLE Estrogen receptor interaction with a transcription factor
 JOURNAL Akzo Nobel N.V. (NL)
 FEATURES Location/Qualifiers B

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 130;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 34 CCTTGAGGGATTCCCTCC 53

RESULT 10
 LOCUS G73338
 DEFINITION G73338 Genomic DNA from human peripheral blood leukocytes Homo
 sapiens STS Genomic 5' and 3', sequence tagged site.

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ACCESSION G73338
 KEYWORDS STS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 397)
 AUTHORS Taylor, J.G., Tang, D., Savage, S., Leitman, S.F., Heller, S.I., Serjeant, G.R., Rodgers, G.P. and Chanock, S.J.
 TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in sickle cell disease
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: ACTGGAACCTGGCTGGGTG
 Primer B: TCACATCAATGCAAACCTGACTG
 STS size: 397
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 72 degrees C for 40 seconds
 Final Extension: 72 degrees C for 600 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 AmpliTaqGold Polymerase: 0.025 units/uL
 Total Vol: 20 uL

Buffer:
 MgCl2 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume

Exon 1 ; The 5' end of PCR primers were tagged with a universal sequencing primer: either M13F (TGTAAAACGACCCGG) for forward primers or M13R (CAGGAACGCTTGTGACC) for reverse primers.

FEATURES
 Source 1. .397
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood leukocytes"
 /note="Human genomic DNA prepared from either fresh or immortalized peripheral blood leukocytes"
 gene 1. .397
 /gene="VCAM1"
 /note="Vascular cell adhesion molecule 1"
 STS 1. .397
 /gene="VCAM1"
 primer_bind 1. .19
 /gene="VCAM1"
 /complement (374. .397)
 primer_bind 1. .397
 /gene="VCAM1"
 ORIGIN Query Match 100.0%; Score 20; DB 11; Length 397;
 Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAAAGGATTCCTTCC 20
 Db 59 CCTTGAAAGGATTCCTTCC 78

RESULT 11
 G73796 LOCUS G73796 Genomic DNA from human peripheral blood leukocytes Homo sapiens STS genomic 5, and 3', sequence tagged site.
 DEFINITION G73796
 ACCESSION G73796.1 GI:27413076
 VERSION 1
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Taylor, J.G., Tang, D., Savage, S., Leitman, S.F., Heller, S.I., Serjeant, G.R., Rodgers, G.P. and Chanock, S.J.
 TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in sickle cell disease
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: TTTTTCTTCCTCCACCCCC
 Primer B: AACCCCTTATTGTGTGTCACCTG
 STS Size: 411
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 63 degrees C for 40 seconds
 Final Extension: 72 degrees C for 400 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 Primer: each 0.5 uM
 dNTPs: 0.025 units/uL
 Total Vol: 20 uL

Buffer:
 MgCl2 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume

5' upstream region.

FEATURES
 Source 1. .411
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood leukocytes"
 /note="Human genomic DNA prepared from either fresh or immortalized peripheral blood leukocytes"
 gene 1. .411
 /gene="VCAM1"
 /note="Vascular cell adhesion molecule 1"
 STS 1. .411
 /gene="VCAM1"
 primer_bind 1. .411
 /gene="VCAM1"
 /complement (389. .411)
 ORIGIN Query Match 100.0%; Score 20; DB 11; Length 411;
 Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 11; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6.8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 262 CCTTGAGGGATTCCCTCC 281

RESULT 12

LOCUS G73795 604 bp DNA linear STS 28-DEC-2002
 DEFINITION Sgg-R136 Genomic DNA from human peripheral blood leukocytes Homo sapiens STS genomic 5' and 3', sequence tagged site.

ACCESSION G73795
 VERSION G73795.1 GI:27413075
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 604)

Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I., Serjeant,G.R., Rodgers,G.P. and Chanock,S.J. TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in sickle cell disease
 Unpublished (2001)

COMMENT Contact: Stephen J. Chanock, Pediatric Oncology Branch, Center for Section of Genomic Variation, National Cancer Institute National Institutes of Health NCI Advanced Technology Center, 8717 Grovemont Circle, Gaithersburg, MD 20871, USA Email: sc83@nih.gov Primer A: GAAAGTATGCTGCCCTTTTTT Primer B: AACCCTATTGTGTCACAC

STS size: 604
 PCR Profile: Preincubation: 95 degrees C for 600 seconds Denaturation: 94 degrees C for 30 seconds Annealing: 55 degrees C for 30 seconds Extension: 72 degrees C for 40 seconds Final Extension: 72 degrees C for 600 seconds 40 PCR Cycles:
 Thermal cycler: MJ Research model PTC-225

Protocol: Template: 10⁻⁵⁰ ng each 0.5 μM
 Primer: dNTPs: each 200 μM
 AmpliTaqGold Polymerase: 0.025 units/ul
 Total Vol: 20 μl

Buffer: MgCl₂ 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume

FEATURES 5' upstream region.
 SOURCE Location/Qualifiers 1..604
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood leukocytes"
 /note="Human genomic DNA prepared from either fresh or immortalized peripheral blood leukocytes"
 1..604 /gene="VCAM1"
 /note="Vascular cell adhesion molecule 1"
 1..604 /gene="VCAM1"
 /gene="VCAM1"
 primer_bind complement (585..604)

ORIGIN Query Match 100.0%; Score 20; DB 10; Length 992;
 Best Local Similarity 100.0%; Pred. No. 6.7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 592 CCTTGAGGGATTCCCTCC 611

RESULT 13

LOCUS MMVCAM1B1 992 bp DNA linear ROD 03-MAY-2000
 DEFINITION Mus musculus NIH Swiss vascular cell adhesion molecule-1 (VCAM-1) gene, exon 1, partial cds.
 ACCESSION U12878
 KEYWORDS 1 of 6
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metacozia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 796; 808 to 824)
 AUTHORS Kumar,A.G., Dai,Y.X., Kozak,C.A., Mims,M.P., Gotto,A.M. and Ballantyne,C.M.

TITLE Murine VCAM-1: Molecular cloning, Mapping, and Analysis of a Truncated Form
 JOURNAL Unpublished
 JOURNAL 2 (bases 1 to 992)
 AUTHORS Kumar,A.G.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-1994) Ajith G. Kumar, Department of Medicine, Baylor College of Medicine, 6555 Fannin Street, Houston, TX 77030, USA
 COMMENT On Oct 28, 1995 this sequence version replaced gi:531856
 FEATURES Location/Qualifiers 1..992
 SOURCE /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /chromosome="3"
 /clone="lambda 1"
 /cell_line="NIH3T3"
 /cell_type="fibroblast"
 /clone_lib="Genomic library lambda FIX II, Stratagene, La Jolla, CA"
 /dev_stage="adult"
 CDS 632..636
 /751..814
 /gene="VCAM-1"
 /codon_start_1
 /product="vascular cell adhesion molecule-1"
 /protein_id="AA806059.1"
 /db_xref="GI:531863"
 /translation="MPVXAVAVGASTVWLFAV"
 sig_peptide 751..814
 exon /gene="VCAM-1"
 /gene="VCAM-1"
 /number=1

ORIGIN Query Match 100.0%; Score 20; DB 10; Length 992;
 Best Local Similarity 100.0%; Pred. No. 6.7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 592 CCTTGAGGGATTCCCTCC 611

AR174653 AR174653 1032 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 8 from patent US 6307025.
 ACCESSION AR174653
 VERSION AR174653.1 GI:17914973
 KEYWORDS Unknown.
 SOURCE ORGANISM Unclassified.
 REFERENCE Hession, C.A., Robb, M.D.
 AUTHORS Goelz, S.E., Osborn, L., Benjamin, C.D. and
 TITLE VCAM fusion proteins and DNA coding therefor
 JOURNAL Patent: US 6307025-A 8 23-OCT-2001;
 FEATURES Location/Qualifiers
 source 1. .1032
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 ORIGIN Query Match 100.0%; Score 20; DB 6;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 221 CCTTGAGGGATTCCCTCC 240

Search completed: December 28, 2004, 10:45:37
 Job time : 178 sec

ORIGIN Query Match 100.0%; Score 20; DB 6;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 221 CCTTGAGGGATTCCCTCC 240

RESULT 15
 BD140422 BD140422 1032 bp DNA linear PAT 18-SEP-2002
 LOCUS Endothelial-leukocyte adhesion molecule (ELAM) and molecule
 DEFINITION Participating in leukocyte adhesion (MILA).
 ACCESSION BD140422
 VERSION BD140422.1 GI:23235367
 KEYWORDS JP 2002065285-A/6.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1032)
 AUTHORS Hession, C.R., Lobb, R.R., Goelz, S.E., Osborn, L., Benjamin, C.D. and
 Rosa, M.D.
 TITLE Endothelial-leukocyte adhesion molecule (ELAM) and molecule
 JOURNAL participating in leukocyte adhesion (MILA)
 Patent: JP 2002065285-A 6 05-MAR-2002;
 BIOPEN INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002065285-A/6
 PD 05-MAR-2002
 PF 18-JUN-2001 JP 20011841133 359516 PR
 PR 28-APR-1989 US 345151,01-JUN-1989 US 359516 PR
 18-DEC-1989 US 452675
 PI CATHERINE R HESSION, ROY E LOBB, SUSAN E GOELZ, LAURELY OSBORNE,
 PI CHRISTOPHER D BENJAMIN, MARGARET D ROSA,
 PC C12N15/09, A61K35/16, A61K38/00, A61K45/00, A61K48/00, A61P/00, PC
 A61P17/00, A61P35/00, C07K14/47, C07K16/18, C07K16/42, C12N1/15, C12N1/19, PC
 PC C12N1/21,
 C12N5/10, C12N5/10, C12N5/10, C12N15/02, C12P21/02, C12P21/08, C1Q1/ PC
 02, G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/566, G01N33/577,
 PC C12N15/00, C12N15/00, C12N5/00, C12N5/00, C12N5/00 CC
 PC C12N5/00, C12N5/00, C12N5/00 CC
 Endothelial-leukocyte adhesion molecule (ELAM) and molecule CC
 Participating
 in leukocyte adhesion (MILA)
 CC in leukocyte adhesion (MILA)
 FH Location/Qualifiers
 FT 1. .1032
 /organism="Homo sapiens (human)"
 FT Location/Qualifiers
 FEATURES

ATTACHMENT S

RESULT 1
 AAT69675 standard; DNA; 20 BP.
 XX
 AC AAT69675;
 XX DT 04-AUG-1997 (first entry)
 XX DE Transcription factor NF-kappa-B DNA binding site antagonist.
 XX KW Decoy; antagonist; NF-kappa-B; NF-kB; transcription; regulation;
 prevention; treatment; disease; ischemia; ischaemia; inflammation;
 KW autimmune; cancer; mettastasis; cachexia; organ; transplantation;
 KW surgery; ds.
 XX OS Synthetic.
 XX PN WO9335430-A1.
 XX PD 14-NOV-1996.
 XX PP 10-MAY-1996; 96WO-JP001234.
 XX PR 12-MAY-1995; 95JP-00114990.
 PR 02-NOV-1995; 95JP-00265504.
 XX PA (FUTI) FUJIWARA PHARM CO LTD.
 XX PI Morishita R, Ogihara T, Sugimoto T, Maeda K, Kawamura I, Chiba T;
 XX WPI: 1996-518100/51.
 XX DR
 XX PT Anti:sense NF-kB agent - for treatment of ischaemia, inflammatory disease
 auto:immune disease, etc.
 PT XX PS Page 9; 18pp; Japanese.
 XX CC The present sequence is a decoy, which specifically antagonises the
 nucleic acid site to which a NF-kappa-B transcription regulator binds. It
 CC can be used to prevent or treat diseases caused by NF-kappa-B. E.g.
 CC ischaemia, inflammatory and autoimmune disease, cancer metastasis and
 CC cachexia, especially following organ transplant or surgery
 XX SOTOMARCO 20 BP. 3. 7. 7. C. A. C. 6. T. 0. U. 0. October.

PrEd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match	Length	DB	ID	Description	
							Transcrip-	Human NF-
1	20	100..0	20	2	AAT69675	Aat69675	Aaa1435	Human NF-
2	20	100..0	20	3	AAA1435	Aaa1435	Aaa1435	Human NF-
3	20	100..0	20	4	AAH43069	Aah43069	Aah43069	Nucleotid
4	20	100..0	20	6	ABV72301	Abv72301	Abv72301	Nucleotid
5	20	100..0	20	6	AB554472	Ab554472	Ab554472	Nuclear F
6	20	100..0	20	9	ACC79778	Acc79778	Acc79778	Nuclear F
7	20	100..0	20	10	ADD69731	Add69731	Add69731	Cerebral
8	20	100..0	20	10	ADPF53868	Adf53868	Adf53868	Circulat
9	20	100..0	20	12	ADG43792	Adg43792	Adg43792	Syntheti
10	20	100..0	20	12	ADFG69331	Adf69331	Adf69331	NF-kappa
11	20	100..0	20	12	ADM91765	Adm91765	Adm91765	C1s elien
12	20	100..0	20	12	ADPB38386	Adpb38386	Adpb38386	Nuclear
13	20	100..0	36	2	AAQ90101	Aaq90101	Aaq90101	VCM-1 ex
14	20	100..0	47	2	AAQ90100	Aaq90100	Aaq90100	VCM-1 ex
15	20	100..0	130	10	ACF79417	Acf79417	Acf79417	VCAM-1 F
16	20	100..0	1024	10	AB283493	Ab283493	Ab283493	Toxicolo
17	20	100..0	1032	2	AAQ06690	Aaq06690	Aaq06690	5' UTR of
18	20	100..0	1032	6	AAS17081	Aas17081	Aas17081	Human vas
19	20	100..0	1032	10	ADHT73058	Adht73058	Adht73058	Human adhe
20	20	100..0	2396	3	AAA34966	Aaa34966	Aaa34966	Human ade
21	20	100..0	2396	3	AAA34967	Aaa34967	Aaa34967	Human ade

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 2
 AAA14365 AAA14365 standard; DNA; 20 BP.
 AC AAA14365;
 XX 15-AUG-2000 (first entry)
 DE Human NF-kappa-B binding site EMSA probe.
 XX NK-kappa-B binding site; nuclear factor-kappa-B; EMSA;
 KW electrophoretic mobility shift assay; advanced glycation end-product;
 KW receptor for AGE; PAGE; interaction inhibitor; kidney failure;
 KW diabetes; systemic lupus erythematosus; inflammatory lupus nephritis;
 KW obesity; amyloidoses; inflammation; ageing; ds.
 XX OS Homo sapiens.
 PN WO20020458-A1.
 XX 13-APR-2000.
 PD XX 05-OCT-1999; 99WO-US0232345.
 PR XX 05-OCT-1998; 98US-00166649.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Schmidt AM, Stern D;
 DR WPI; 2000-303750/26.
 PT Determining inhibitors of interaction between an advanced glycation endproduct and its receptor, useful to develop therapeutics for various associated conditions including diabetes and inflammatory lupus nephritis.
 PT WPI; 2000-303750/26.
 XX PS Example 1; Page 30; 66pp; English.
 XX The invention relates to a novel method for determining whether a compound can inhibit interaction of an advanced glycation end-product (AGE) or fragment thereof with the receptor for AGEs (RAGE). The method comprises admixing the AGE (which has its amino groups inactivated by chemical derivatization), RAGE, and the compound, determining the amount of peptide bound to RAGE, and comparing this amount to the amount of peptide binding in the absence of the compound. A decrease in AGE/RAGE binding in the presence of the compound indicates that the compound is an inhibitor. Exemplary inhibitor compounds identified via the method are quinines, quinidine, or derivatives with the same overall charge as these compounds. AGEs are a class of compounds with heterogeneous structures that result from the process of glycoxidation. The accumulation of AGEs has been linked to a range of complications that occur in disorders such as ageing, diabetes, renal failure and inflammation. Interaction of an AGE with RAGE triggers multiple mechanisms, including the activation of NF-kappa-B (nuclear factor kappa-B), which result in cellular perturbation and dysfunction. Compounds which inhibit the interaction between AGEs and RAGE may be used to treat kidney failure, diabetes, systemic lupus erythematosus, inflammatory lupus nephritis, obesity, amyloidoses or inflammation. Administration of such compounds may also be of benefit to elderly individuals, particularly humans, other primates, mice, rats or dogs. The present sequence represents an NF-kappa B binding site probe used in electrophoretic mobility shift assays (EMSA) of nuclear extracts of human umbilical vein endothelial cells (HUVECs) previously treated

CC with an AGE
 XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 3
 AAH43069 AAH43069 standard; DNA; 20 BP.
 ID AAH43069;
 AC AAH43069;
 XX 15-OCT-2001 (first entry)
 DE Nucleotide sequence of an oligonucleotide hybridizing to HVJ.
 KW Gene insertion vector; virus envelope; gene therapy; HVJ; ss.
 XX Unidentified.
 OS XX Key Location/Qualifiers
 FH 1
 FT modified_base 1
 FT /*tag= "a"
 FT /note= "FIRIC attached"
 XX PN WO200157204-A1.
 PD 09-AUG-2001.
 PR 02-FEBB-2001; 2001WO-JP000782.
 PR 02-FEBB-2000; 2000JP-00025596.
 PR XX (KANEKA) KANEDA Y.
 PA XX (KANEKA) KANEDA Y.
 PI XX
 DR WPI; 2001-496921/54.
 PT Virus envelope vector used in gene transfer for gene therapy in a broad range of tissues.
 XX PT
 PS Example 4; Page 32-33; 75pp; Japanese.
 XX The specification describes a gene insertion vector, consisting of a virus envelope into which the gene to be transferred can be inserted. The virus envelope is transferred into an inactivated virus envelope by the foreign gene is transferred into an inactivated virus envelope by the freezing and thawing method or by mixing a surfactant. The gene insertion vector is used for high efficiency gene therapy in a broad range of animal tissues such as lung, bone, ovary, brain, nerve, eye, skin, blood vessel, liver, heart, kidney, spleen, B-lymphocyte, or cancerous tissue. The present sequence represents an oligonucleotide which hybridizes to HVJ. It is used in the course of the invention.

CC Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 4

XX The present invention describes pharmaceutical compositions (A) for
 CC inhibiting rejection in organ transplantation which contain a nuclear
 CC factor-kappa B (NF-kappa-B) decoy compound. Also described: (1) a method
 CC for inhibiting rejection in organ transplantation by administering of the decoy
 CC remedies (A) to a donor organ before ultrasonication of the decoy
 CC compound-containing donor organ; (2) a method for improving prognosis of
 CC organ transplantation by administering any of the remedies (A) to a donor
 CC organ before ultrasonication of the decoy compound containing donor organ
 CC and (3) a method for elevating transfection of an oligonucleotide into
 CC a biological tissue by administering such oligonucleotide to a donor
 CC organ before ultrasonication of the oligonucleotide-containing biological
 CC tissue. (A) have immunosuppressive activity, and can be used in NF-kappa-
 B inhibitors. The remedies (A) can be used in regeneration and
 CC transplantation medicine. Specifically, they are for inhibiting rejection
 CC in organ transplantation and improving its prognosis, particularly kidney
 CC transplants. The present sequence represents an NF-kappa-B decoy
 CC oligonucleotide, which is used in an example from the present invention
 XX

Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Gaps 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGATTCCCTCC 20
 Db 1 CCTTGAAGGATTCCCTCC 20

RESULT 7
 ADD9731 Standard; DNA; 20 BP.
 XX
 AC
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Cerebral ischaemia-related NF-kappaB decoy DNA.

XX cerebral ischaemia; nuclear factor kappaB; NF-kB decoy; neuroprotective;
 XX nootropic; cerebroprotective; brain tumour; nerve injury;
 XX sub-cranial membrane bleeding; hypertensive intracranial; infarction;
 XX chronic; acute subdural haematoma; ds.
 XX Unidentified.
 XX
 PN WO2003082331-A1.
 XX
 PD 09-OCT-2003.
 XX
 PR 29-MAR-2002; 2002WO-JP003239.
 XX
 PR 29-MAR-2002; 2002WO-JP003239.
 XX
 PA (ANGE) ANGES MG INC.
 PA (SAWA) SAWA Y.

XX Sawa Y, Morishita R, Kaneda Y, Matsuda H, Yoshimine T;
 XX PI; 2003-812503/76.
 DR

XX Transfection of NF-kB decoy oligonucleotide into brain tissue by carotid
 PR injection using a suitable carrier for treatment and prevention of
 PT disorders associated with cerebral ischemia.
 XX
 PS Example 1; SEQ ID NO 1; 79pp; Japanese.

XX The invention relates to a novel drug composition for prevention and treatment of disorders associated with cerebral ischaemia which contains a nuclear factor kappaB (NF-kB) decoy oligonucleotide together with a suitable carrier for its transfection. The composition of the invention demonstrates neuroprotective, nootropic and cerebroprotective activities

CC and may be useful for the prevention of brain and nerve injury following
 CC disorders associated with cerebral ischaemia, such as sub-cranial
 CC membrane bleeding, hypertensive intracranial bleeding, cerebral
 CC infarction, brain tumour or chronic or acute subdural haematoma. The
 CC current sequence is that of the cerebral ischaemia-related NF-kappaB
 CC decoy DNA of the invention.

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Gaps 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAAGGATTCCCTCC 20
 Db 1 CCTTGAAGGATTCCCTCC 20

RESULT 8
 ADF53868
 ID ADF53868 Standard; DNA; 20 BP.
 XX
 AC ADF53868;
 XX DT 12-FEB-2004 (first entry)
 XX DE Circular dumbbell oligodeoxynucleotide related oligo, SEQ ID No 9.
 XX circular dumbbell oligodeoxynucleotide; CDODN; DNA-binding domain;
 KW transcriptional factor; vasotropic; antiinflammatory; gastrointestinal;
 KW dermatological; antiarteriosclerotic; antiatherosclerotic; cyostatic;
 KW antiasthmatic; gene therapy; Ap-1 decoy; B2F decoy;
 KW vascular smooth muscle cell proliferation; neointimal hyperplasia;
 KW restenosis; prophylaxis; exonuclease; ss.
 XX Unidentified.
 XX
 OS WO2003091432-A1.
 XX
 OS Unidentified.
 XX
 PN WO2003091432-A1.
 XX
 PD 06-NOV-2003.
 XX
 PR 26-APR-2002; 2002WO-JP004303.
 XX
 PR 26-APR-2002; 2002WO-JP004303.
 XX
 PR (ANGE) ANGES MG INC.
 PA (LEE) / LEE I.
 XX
 PR Lee I, Morishita R;
 XX
 DR WPI: 2003-877331/81.
 XX
 PT New circular dumbbell oligonucleotide comprising two loops and a stem
 PT structure capable of binding the DNA-binding domain of Ap-1, E2F or
 PT NEkappaB useful in treating or preventing vascular smooth muscle cell
 PT proliferation.

XX Disclosure; SEQ ID NO 9; 142pp; English.
 XX
 CC The invention relates to a novel circular dumbbell oligodeoxynucleotide
 CC (CDODN) comprising two loop structures and a stem structure, where the
 CC stem structure comprises a nucleotide sequence capable of binding the DNA
 CC -binding domain of a transcriptional factor. The invention further
 CC comprises: a method for treating or preventing a disease or disorder
 CC related to a transcription or preventing a disease or disorder related to a
 CC transcriptional factor in a subject, and a pharmaceutical
 CC composition for treating or preventing a disease or disorder comprising a therapeutic amount of a
 CC CDODN described above and a pharmaceutical carrier. The CDODN oligo has
 CC the following activities: vasotropic, antiinflammatory, gastrointestinal,
 CC dermatological, antiarteriosclerotic, antiatherosclerotic, cyostatic, and
 CC antiasthmatic. The CDODN can be used in gene therapy. The CDODN are
 CC used in the manufacture of a medicament for treating or preventing a
 CC disease or disorder related to a transcriptional factor in a subject. The
 CC

CC CDDON or the composition or the AP-1 decoy or E2F decoy is useful in
 CC treating or preventing a disease or disorder related to a transcriptional
 CC factor, e.g. vascular smooth muscle cell proliferation, neointimal
 CC hyperplasia following vessel injury or inflammatory bowel disease or in
 CC preventing restenosis and used in prophylaxis. Further diseases/disorders
 CC include inflammatory disease, dermatitis, aneurism, arteriosclerosis,
 CC atherosclerosis, angitis, cancer or asthma. The AP-1 decoy
 CC oligonucleotide with a CDDON is useful to avoid destruction by
 CC exonucleases. This sequence represents a circular dumbbell
 CC oligodeoxynucleotide related oligo of the invention.

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 ID 1 ADG43792 standard; DNA; 20 BP.
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 9
 Synthetic NF-kappaB decoy SEQ ID NO:1.

XX NF-kappaB; cerebroprotective; cytostatic; ophthalmological; osteopathic;
 KW antiarthritic; antiallergic; dermatological; nephrotoxic; periodontal;
 KW cerebral aneurysm; cancer; Marfan's syndrome; arctic dissection;
 KW postangioplasty reconstruction; rheumatoid arthritis; asthma;
 KW atopic dermatitis; renal insufficiency; plaque rupture; ss; ets.
 XX Synthetic.
 OS WO2003063911-A1.
 XX 07-AUG-2003.
 XX 01-FEB-2002; 2002WO-JP000865.
 PR 01-FEB-2002; 2002WO-JP000865.
 XX (ANGE-) ANGES MG INC.

XX Morishita R, Aoki M, Ogihara T, Kawasaki T;
 PI 2003-748040/70.
 XX Composition for treating and preventing diseases caused by the expression
 PT of gene under regulation of NF-kappaB or ets comprises decoy and carrier.
 XX Example 2, Page 19; 46pp; Japanese.

CC The invention relates to a novel composition for treating and preventing
 CC diseases caused by the expression of a gene under the regulation of NF-
 CC kappaB or ets comprises at least one decoy and a carrier. A composition
 CC of the invention has cerebroprotective, cytostatic, ophthalmological,
 CC osteopathic, antiarthritic, antiallergic, dermatological, nephrotoxic,
 CC and periodontal activity. The composition is useful for treating and
 CC preventing diseases caused by the expression of a gene under the
 PT regulation of NF-kappaB or ets such cerebral aneurysm, cancer, Marfan's
 CC syndrome, aortic dissection, postangioplasty reconstruction, rheumatoid
 CC arthritis, asthma, atopic dermatitis. Renal insufficiency and plaque
 CC rupture. The present sequence represents an NF-kappaB decoy of the
 CC invention.
 XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 10
 Synthetic NF-kappaB decoy SEQ ID NO:1.
 XX NF-kappaB standard; DNA; 20 BP.
 AC ADG9631;
 XX 26-FEB-2004 (first entry)
 DB NF-kappaB binding site as decoy for inflammatory disease.
 XX
 KW SS; antiinflammatory; antiarthritic; antirheumatic; antiarteriosclerotic;
 KW nephrotoxic; inflammatory disease; joint disease;
 KW NF-kappa B binding site; nephritis; hepatitis; renal failure;
 KW arteriosclerosis; Glomerulonephritis; Pyelonephritis; Cystitis;
 KW prostatitis; urethritis; epididymitis; testitis; arthritis deformans;
 KW rheumatoid arthritis; periarthritis of shoulder;
 KW neck-shoulder-wrist syndrome.
 XX Home sapiens.
 OS WO2003063911-A1.
 XX 04-DEC-2003.
 PD 20-MAY-2003; 2003WO-JP006299.
 PR 29-MAY-2002; 2002JP-00156524.
 XX (ANGE-) ANGES MG INC.
 PA PI Tomita T, Yoshikawa H, Morishita R;
 XX WO2003063911-A1.
 DR WPI; 2004-023234/02.
 XX Remedies or preventing for inflammatory or joint diseases and disorders,
 PT e.g. rheumatoid arthritis, arthritis deformans and nephritis, containing
 PT decoy of NF-kappa B or analogous transcriptional factor.
 XX Disclosure; SEQ ID NO 1; 82pp; Japanese.

XX The invention relates to a drug composition for treating or preventing
 CC inflammatory or joint disease or disorders comprising at least 1 decoy of
 CC NF-kappa B binding site. The NF-kappa B decoy is preferably the
 CC nucleotide sequence GGATTCCCC. The drugs are for inflammatory diseases
 CC and disorders, including nephritis, hepatitis, arthritis, acute/chronic
 CC renal failure, arteriosclerosis, glomerulonephritis, pyelonephritis,
 CC cystitis, prostatitis, urethritis, epididymitis and testitis,
 CC particularly arthritis deformans or rheumatoid arthritis, especially
 CC -wrist syndrome and secondary arthritis. This sequence corresponds to
 CC the NF-kappa B decoy.

Query Match 100.0%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 11

ADM91765 ID ADM91765 standard; DNA; 20 BP.
 XX AC ADM91765;
 XX DT 17-JUN-2004 (first entry)
 XX DB Cis element decoy oligonucleotide #2.
 XX PR transplanted blood vessel; transcription factor; NF kappa-B; cis element;
 XX KW oligonucleotide; 85.
 XX OS Synthetic.
 XX PN WO2004026342-A1.
 XX PD 01-APR-2004.
 XX PR 27-DEC-2002; 2002WO-JP013805.
 XX PR 20-SEP-2002; 2002JP-00275884.
 XX PA (ANGE-) ANGES MG INC.
 XX PI Sawa Y., Shintani T., Matsuda H.;
 XX DR WPI; 2004-295314/27.
 XX PT Method for controlling transcription transplanted blood vessels induced
 XX by NF kappa-B for preventing thickening.
 XX Disclosure; SEQ ID NO 2; 31PP; Japanese.
 XX The present invention relates to the method for controlling transcription
 CC of blood vessels or transplanted blood vessels activated by transcription
 CC factor NF kappa-B by placing them in contact with a decoy against NF
 CC kappa-B. The method is used for preventing thickening in transplanted
 CC blood vessels. The present sequence represents a cis element decoy
 CC oligonucleotide.
 XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 XX SQ Query Match 100.0%; Score 20; DB 12; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.9;
 XX Matches 20; Conservative 0; Mismatches 0; Gaps 0;
 XX Indels 0;
 XX QY 1 CCTTGAGGGATTCCCTCC 20
 XX 1 CCTTGAGGGATTCCCTCC 20
 XX Db 1 CCTTGAGGGATTCCCTCC 20
 XX
 XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 XX SQ Query Match 100.0%; Score 20; DB 12; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.9;
 XX Matches 20; Conservative 0; Mismatches 0; Gaps 0;
 XX Indels 0;
 XX QY 1 CCTTGAGGGATTCCCTCC 20
 XX 1 CCTTGAGGGATTCCCTCC 20
 XX Db 1 CCTTGAGGGATTCCCTCC 20
 XX
 RESULT 12

ADP83986 ID ADP83986 standard; DNA; 20 BP.
 XX AC ADP83986;
 XX DT 26-AUG-2004 (first entry)
 XX Nuclear factor-kappaB decoy oligonucleotide #1.
 XX DB Nuclear factor-kappaB; NF kappaB; ets; cerebral aneurysm; cancer;
 XX KW Marfan's syndrome; aortic detachment; post-angioplasty restenosis;
 XX KW chronic articular rheumatism; asthma; atopic dermatitis; nephritis;
 XX KW renal failure; plaque rupture; plaque; atherosclerosis; inflammatory disease; 65.
 XX KW transcriptional regulatory factor; diagnosis; treatment; restenosis;
 XX KW bronchial asthma; childhood asthma; allergic asthma; atopic asthma;
 XX KW steroid-resistant asthma; SRA; non-allergic asthma; intrinsic asthma;
 XX KW extrinsic asthma; aspirin-induced asthma; cardiac asthma;
 XX KW infectious asthma; allergy; skin disease; mycosis; vaccine; therapy; 66.
 XX OS Unidentified.
 XX PD 11-MAY-1995.

RESULT 13

AAQ90101 ID AAQ90101 standard; DNA; 36 BP.
 XX AC AAQ90101;
 XX DT 11-JAN-1996 (first entry)
 XX VCAM-1 expression inhibiting oligonucleotide.
 XX DB VCAM-1 expression inhibiting oligonucleotide.
 XX KW vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
 XX KW transcriptional regulatory factor; diagnosis; treatment; restenosis;
 XX KW atherosclerosis; inflammatory disease; 65.
 XX OS Synthetic.
 XX PN WO9512415-A1.
 XX PD 11-MAY-1995.

XX 07-NOV-1994; 94WO-US012797.
 XX PR 05-NOV-1993; 93US-00147878.
 XX PA (ISIS-) ISIS PHARM INC.
 PA (UYEM-) UNIV EMORY.
 XX PI Medford RM, Bennett CF;
 XX DR WPI; 1995-193802/25.
 XX Oligo-nucleotide(s) which modulate vascular cell adhesion molecule expression by binding a transcription regulatory element - used to diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 XX PS Claim 17; Page 33; 49pp; English.
 XX AAQ90100-090111 bind the vascular cell adhesion molecule (VCAM)-1 gene transcriptional regulatory factor, therefore inhibiting the expression of VCAM-1. They can be used in the diagnosis and treatment of restenosis, atherosclerosis and inflammatory diseases
 XX SQ Sequence 36 BP; 3 A; 13 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 XX PS 1 CCTTGAGGGATTCCCTCC 20
 DB 16 CCTTGAGGGATTCCCTCC 35

RESULT 14
 AAQ90100
 ID AAQ90100 standard; DNA; 47 BP.
 XX AC AAQ90100;
 XX DT 11-JAN-1996 (First entry)
 DE VCAM-1 expression inhibiting oligonucleotide.
 XX KW Vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
 KW transmembrane regulatory factor; diagnosis; treatment; restenosis;
 KW atherosclerosis; inflammatory disease; ds.
 XX OS Synthetic.
 XX PN WO9512415-A1.
 XX PD 11-MAY-1995.
 XX PR 07-NOV-1994; 94WO-US012797.
 XX PR 05-NOV-1993; 93US-00147878.
 XX PA (ISIS-) ISIS PHARM INC.
 PA (UYEM-) UNIV EMORY.
 XX PI Medford RM, Bennett CF;
 XX DR WPI; 1995-193802/25.
 XX Oligo-nucleotide(s) which modulate vascular cell adhesion molecule expression by binding a transcription regulatory element - used to diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 XX PS Claim 17; Page 33; 49pp; English.
 XX CC AAQ90100-090111 bind the vascular cell adhesion molecule (VCAM)-1 gene transcriptional regulatory factor, therefore inhibiting the expression of

CC VCAM-1. They can be used in the diagnosis and treatment of restenosis, atherosclerosis and inflammatory diseases
 XX SQ Sequence 47 BP; 3 A; 17 C; 12 G; 15 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 22 CCTTGAGGGATTCCCTCC 41

RESULT 15
 ID ACP79417 standard; DNA; 130 BP.
 XX ACP79417;
 AC ACP79417;
 XX DT 18-DEC-2003 (first entry)
 DE VCAM-1 promoter.
 XX KW VCAM-1; promoter; oestrogen; receptor; c-rel; osteoporosis; osteopathic;
 KW ds.
 XX PS Location/Qualifiers
 FH 26 .35
 PT /*tag= a
 PT /bound_moiety= "Nuclear factor-kappaB"
 PT protein_bind
 PT 40 .50
 PT /*tag= b
 PT /bound_moiety= "Nuclear factor-kappaB"
 XX WO2003071281-A2.
 XX PD 28-AUG-2003.
 XX PP 21-FEB-2003; 2003WO-EP050027.
 XX PR 25-FEB-2002; 2002EP-00075789.
 PA (ALIKU) AKZO NOBEL NV.
 PI Boerema CJC, Van Gool AJ;
 XX DR WPI; 2003-748205/70.
 XX PS Example; Page 32; 38pp; English.
 XX PT Measuring a direct interaction between an estrogen receptor and c-Rel in an in vitro system, for selecting a compound to treat osteoporosis, by providing for a detection parameter proportionally related to the degree of the interaction.
 XX PR CC The present sequence in that of a cloned selection of the promoter region of the VCAM-1 gene. The promoter contains nuclear factor-kappaB response elements. The invention provides a method to measure a direct interaction between an estrogen receptor and a transactivation protein (c-Rel) in an in vitro system by providing for a detection parameter proportionally related to the degree of the interaction. A yeast two-hybrid assay for the measurement is provided. The detection parameter, i.e. the method used to measure the interaction, includes the use of promoter reporter constructs that contain NF-kappaB or oestrogen receptor responsive regulatory elements fused to a heterologous reporter gene capable of signalling the activation of the regulatory element. The method is useful for selecting a compound for therapeutic efficacy in osteoporosis
 XX SQ Sequence 130 BP; 23 A; 43 C; 24 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTGAGGAGTTCCCTCC 20
Db 34 CCTTGAGGAGTTCCCTCC 53

Search completed: December 28, 2004, 10:15:52
Job time : 4.04 secB

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	20	3	US-08-945-805-1	Sequence 1, APP1	Sequence 1, APP1
2	20	100.0	20	4	US-08-945-805-1	Sequence 1, APP1	Sequence 1, APP1
3	20	100.0	36	4	US-08-945-805-1	Sequence 1, APP1	Sequence 1, APP1
4	20	100.0	46	4	US-08-945-805-1	Sequence 1, APP1	Sequence 1, APP1
5	20	100.0	1032	3	US-08-945-805-1	Sequence 8, APP1	Sequence 8, APP1
6	18	90.0	19	4	US-08-945-805-1	Sequence 4, APP1	Sequence 4, APP1
c 7	16.8	84.0	32	4	US-08-945-805-1	Sequence 1506, APP1	Sequence 1506, APP1
c 8	16.8	84.0	32	4	US-08-945-805-1	Sequence 1506, APP1	Sequence 1506, APP1
c 9	16.8	84.0	47	4	US-08-945-805-1	Sequence 39, APP1	Sequence 39, APP1
c 10	16.8	84.0	47	4	US-08-945-805-1	Sequence 40, APP1	Sequence 40, APP1
c 11	16.8	84.0	47	4	US-08-945-805-1	Sequence 41, APP1	Sequence 41, APP1
c 12	16.8	84.0	47	4	US-08-945-805-1	Sequence 42, APP1	Sequence 42, APP1
c 13	16.8	84.0	47	4	US-08-945-805-1	Sequence 43, APP1	Sequence 43, APP1
c 14	16.8	84.0	47	4	US-08-945-805-1	Sequence 44, APP1	Sequence 44, APP1
c 15	16.8	84.0	47	4	US-08-945-805-1	Sequence 45, APP1	Sequence 45, APP1
c 16	16.8	84.0	47	4	US-08-945-805-1	Sequence 46, APP1	Sequence 46, APP1
c 17	16.8	84.0	47	4	US-08-945-805-1	Sequence 47, APP1	Sequence 47, APP1
c 18	16.8	84.0	47	4	US-08-945-805-1	Sequence 48, APP1	Sequence 48, APP1
c 19	16.8	84.0	47	4	US-08-945-805-1	Sequence 49, APP1	Sequence 49, APP1
c 20	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 21	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 22	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 23	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 24	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 25	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 26	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1
c 27	16.8	84.0	47	4	US-08-945-805-1	US-08-945-805-1	US-08-945-805-1

ALIGNMENTS

RESULT 1	US-08-945-805-1	Sequence 1, Application US/08945805A	Patent No. 6262033
GENERAL INFORMATION:			
; APPLICANT: MORISHITA, RYUICHI	; APPLICANT: OGAWA, TOSHIO	; APPLICANT: SUGIMOTO, TOSHIKO	; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWANURA, IKUO	; APPLICANT: CHIBA, TOSHIYUKI	; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB	; FILE REFERENCE: 18933-0PCT
; CURRENT APPLICATION NUMBER: US/08/945,805A	; CURRENT APPLICATION NUMBER: 1898-01-06	; EARLIER APPLICATION NUMBER: PCT/JP96/01234	; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1	; LENGTH: 20	; SOFTWARE: PatentIn Ver. 2.0	; SEQ ID NO 1
; TYPE: DNA	; FEATURE: ORGANISM: Artificial Sequence	; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA	; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; US-08-945-805-1	; Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0; Missmatches 0; Indels 0; Gaps 0;	; Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0; Missmatches 0; Indels 0; Gaps 0;	; Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
; Qy 1 CCTCTAAGGGATTCCCTCC 20	; Db 1 CCTCTAAGGGATTCCCTCC 20	; Qy 1 CCTCTAAGGGATTCCCTCC 20	; Db 1 CCTCTAAGGGATTCCCTCC 20
RESULT 2			
; Sequence 1, Application US/09166649B	; Sequence 1, Application US/09166649B	; Sequence 1, Application US/09166649B	; Sequence 1, Application US/09166649B
; Patent No. 6753150	; Patent No. 6753150	; Patent No. 6753150	; Patent No. 6753150
; GENERAL INFORMATION:	; GENERAL INFORMATION:	; GENERAL INFORMATION:	; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York	; APPLICANT: The Trustees of Columbia University in the City of New York	; APPLICANT: Schmidt, Ann Marie	; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M	; APPLICANT: Stern, David M	; APPLICANT: Stern, David M	; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING A PEPTIDE WITH RAGE	; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING A PEPTIDE WITH RAGE	; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING A PEPTIDE WITH RAGE	; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING A PEPTIDE WITH RAGE
; FILE REFERENCE: 56613	; FILE REFERENCE: 56613	; FILE REFERENCE: 56613	; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/09/166,649B	; CURRENT APPLICATION NUMBER: US/09/166,649B	; CURRENT APPLICATION NUMBER: US/09/166,649B	; CURRENT APPLICATION NUMBER: US/09/166,649B
; NUMBER OF SEQ ID NOS: 1	; NUMBER OF SEQ ID NOS: 1	; NUMBER OF SEQ ID NOS: 1	; NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 1 LENGTH: 20 TYPE: DNA ORGANISM: human

FEATURE: NAME/KEY: Primer LOCATION: (1)..(20) OTHER INFORMATION: Primer Against Human NF-kB

FEATURE: NAME/KEY: Primer LOCATION: (1)..(20) OTHER INFORMATION: PCR Primer Against Human NF-kB

US-09-166-649B-1

Query Match Score 20; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAAGGATTCCCTCC 20

Db 1 CCTTGAAAGGATTCCCTCC 20

RESULT 3 US-08-401-192-2

Sequence 2, Application US/08401192

Patent No. 6713621

GENERAL INFORMATION:

APPLICANT: Bennett and Medford

TITLE OF INVENTION: Modulation of selected Gene Expression Through No. 6713621el Oligonucleotide Interaction

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6713621el STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401-192

FILING DATE: 09-Mar-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/147-878

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: John W. Caldwell

REGISTRATION NUMBER: 28,937

REFERENCE/DOCKET NUMBER: ISIS-1021

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 46

STRANDEDNESS: Double

TOPOLogy: Linear

ANTI-SENSE: No

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-08-401-192-1

Query Match Score 20; DB 4; Length 46; Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAAGGATTCCCTCC 20

Db 21 CCTTGAAAGGATTCCCTCC 40

RESULT 5 US-08-482-073-8

Sequence 8, Application US/08482073

Patent No. 6301025

GENERAL INFORMATION:

APPLICANT: Hession, Catherine A.

APPLICANT: Lobb, Roy R.

APPLICANT: Goetz, Susan E.

APPLICANT: Osborn, Lauree

APPLICANT: Benjamin, Christopher D.

APPLICANT: Rosa, Margaret D.

TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION

US-08-401-192-2

Query Match Score 20; DB 4; Length 36; Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAAGGATTCCCTCC 20

Db 21 CCTTGAAAGGATTCCCTCC 40

TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
 TITLE OF INVENTION: ADHESION (MILAB)
 NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Neve
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,073
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: US/08/486,336
 FILING DATE:
 APPLICATION NUMBER: US 07/608298
 FILING DATE: 31-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US 90/02357
 FILING DATE: 27-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/452675
 FILING DATE: 18-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/359516
 FILING DATE: 01-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/354151
 FILING DATE: 28-APR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B124CIP4
 TELEPHONE: (212) 596-9000
 TELEX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 8:
 LENGTH: 1032 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-482-073-8

Query Match 100.0%; Score 20; DB 3; Length 1032;
 Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;

Db 221 CCTTGAGGGATTCCCTCC 240

RESULT 6
 US-08-401-192-4
 Sequence 4, Application US/08401192
 Patent No. 6713621
 GENERAL INFORMATION:
 APPLICANT: Bennett and Medford
 TITLE OF INVENTION: Modulation of selected Gene Expression
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6713621iris

STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/401,192
 FILING DATE: 09-Mar-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/147,878
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Caldwell
 REGISTRATION NUMBER: 28,937
 REFERENCE/DOCKET NUMBER: ISIS-1021
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 ANTI-SENSE: No
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-08-401-192-4

Query Match 90.0%; Score 18; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2%; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTGAGGGATTCCCTCC 20
 Db 1 TTGAGGGATTCCCTCC 18

RESULT 7
 US-09-474-432B-1507/c
 Sequence 157, Application US/09474432B
 Patent No. 6528640
 GENERAL INFORMATION:
 APPLICANT: Riboxyme Pharmaceuticals, Inc.
 APPLICANT: Beigelman, Leo
 APPLICANT: Burgin, Alex
 APPLICANT: Beaudry, Amber
 APPLICANT: Karcishevsky, Alex
 APPLICANT: Adamic, Jasenka
 APPLICANT: Sweeney, David
 APPLICANT: Zirman, Shawn
 TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
 FILE REFERENCE: MBHB0-831-B (247/26)
 CURRENT APPLICATION NUMBER: US 09/474,432B
 PRIOR APPLICATION NUMBER: US 60/064,866
 PRIOR FILING DATE: 1997-11-05
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: US 09/474,432B
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: US 09/301,511
 PRIOR FILING DATE: 1999-04-28
 NUMBER OF SEQ ID NOS: 1526
 SOFTWARE: PatentIn Version 3.0
 SEQ ID NO 1507
 LENGTH: 32
 TYPE: RNA

ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Enzymatic Nucleic Acid
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 NAME/KEY: misc_feature
 LOCATION: (2)..(11)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc_feature
 LOCATION: (12)..(16)
 OTHER INFORMATION: 2'-O-Methyl
 NAME/KEY: misc_feature
 LOCATION: (12)..(16)
 OTHER INFORMATION: 2'-deoxy-2'-amino
 NAME/KEY: misc_feature
 LOCATION: (24)..(24)
 OTHER INFORMATION: 2'-deoxy-2'-amino
 NAME/KEY: misc_feature
 LOCATION: (27)..(29)
 OTHER INFORMATION: 2'-deoxy-2'-amino
 US-09-474-432B-1507

Query Match 84.0%; Score 16.8; DB 4; Length 32;
 Best Local Similarity 90.0%; Pred. No. 6;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
 US-09-474-432B-39/c
 ; Sequence 39, Application US/09474432B
 ; Patent No. 6538640
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Beigelman, Leo
 ; APPLICANT: Burgin, Alex
 ; APPLICANT: Beaudry, Amber
 ; APPLICANT: Karpieky, Alex
 ; APPLICANT: Adamic, Jasenka
 ; APPLICANT: Sneedler, David
 ; APPLICANT: Zinnen, Shawn
 ; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
 ; FILE REFERENCE: MBIB00-831-B (247/276)
 ; CURRENT APPLICATION NUMBER: US/09/474-432B
 ; CURRENT FILING DATE: 1999-12-19
 ; PRIOR APPLICATION NUMBER: US 60/064,866
 ; PRIOR FILING DATE: 1997-11-05
 ; PRIOR APPLICATION NUMBER: US 60/084,727
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: US 09/186,675
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: US 09/301,511
 ; PRIOR FILING DATE: 1999-04-28
 ; NUMBER OF SEQ ID NOS: 1526
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 39
 ; LENGTH: 47
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(10)
 ; OTHER INFORMATION: 2'-O-Methyl
 ; NAME/KEY: misc_feature
 ; LOCATION: (12)..(21)
 ; OTHER INFORMATION: 2'-O-Methyl
 ; NAME/KEY: misc_feature
 ; LOCATION: (43)..(47)
 ; OTHER INFORMATION: 2'-O-Methyl
 ; NAME/KEY: misc_feature
 ; LOCATION: (22)..(26)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (32)..(32)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (34)..(35)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (37)..(39)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (47)..(47)
 ; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in
 ; US-09-474-432B-39

Query Match 84.0%; Score 16.8; DB 4; Length 47;
 Best Local Similarity 90.0%; Pred. No. 6;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-476-387-1506/c

Query Match 84.0%; Score 16.8; DB 4; Length 32;
 Best Local Similarity 90.0%; Pred. No. 6;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 US-09-476-387-1506/c
 ; Sequence 1506, Application US/09476387
 ; Patent No. 661438
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Beigelman, Leo
 ; APPLICANT: Beaudry, Amber
 ; APPLICANT: Karpieky, Alex
 ; APPLICANT: Adamic, Jasenka Matulic
 ; APPLICANT: Sneedler, Dave
 ; APPLICANT: Zinnen, Shawn
 ; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into Oligonucleot
 ; FILE REFERENCE: MBIB00-831-C (249/073)
 ; CURRENT APPLICATION NUMBER: US/09/476,387
 ; PRIOR APPLICATION NUMBER: 09/474,432
 ; PRIOR APPLICATION NUMBER: 09/301,511
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR FILING DATE: 60/083,727
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR FILING DATE: 1997-11-05
 ; NUMBER OF SEQ ID NOS: 1524
 ; SOFTWARE: PatentIn version 3.0
 ; LENGTH: 32
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ; NAME/KEY: misc_feature
 ; LOCATION: (2)..(11)
 ; OTHER INFORMATION: 2'-O-Methyl
 ; NAME/KEY: misc_feature
 ; LOCATION: (12)..(16)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (24)..(24)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; LOCATION: (27)..(29)
 ; OTHER INFORMATION: 2'-deoxy-2'-amino
 ; NAME/KEY: misc_feature
 ; LOCATION: (47)..(47)
 ; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in
 ; US-09-476-387-1506

Qy	1	CCTTGAAGGGATTTCCCTCC	20
	30	CCTTGAAGGGAGTTCCCTCC	11
Db			

RESULT 11
US-09-474-432B-41/C
Sequence 41, Application US/09474432B

RESULT 10
US-09-474-432B-40/C

OTHER INFORMATION: 2'-deoxy-2'-amin
NAME KEY: misc feature
LOCATION: (47)_.(47)
OTHER INFORMATION: 3'-end phosphate
US-09-474-432B-40

Query	Match	Score	DB 4 ;	Length
Best	Local	84.0% ;	16.8 ;	47 ;
Best	Local	90.0% ;	Pred. No. 6.6 ;	

US-19-4/4-432B-40 Query Match 84.0% ; Score
 Best Local Similarity 90.0% ; Pred.
 Matches 18 ; Conservative 0 ; Mi

Qy	1	CCCTGAAAGGATTCCCTCC	2.0
Db	3.0	CCCTGAAAGGAGTTCCCTCC	1.1

RESULT 12
US-09-474-432B-42/C
; Sequence 42, Application US/09474432B
; Patent No. 6528640
; Computer INFORMATION

CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 1526
SEQ ID NO: 44
LENGTH: 47
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
NAME/KEY: misc_feature
LOCATION: (1)..(10)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc_feature
LOCATION: (12)..(21)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc_feature
LOCATION: (43)..(47)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc_feature
LOCATION: (22)..(26)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc_feature
LOCATION: (32)..(32)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc_feature
LOCATION: (34)..(35)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc_feature
LOCATION: (37)..(39)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc_feature
LOCATION: (47)..(47)
OTHER INFORMATION: 3'-end phosphate attach

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Query Match      84.0%;  Score 16.8;  DB 4;  Length 47;
Best Local Similarity 90.0%;  Pred. No. 6.6;
Matches 18;  Conservative 0;  Mismatches 2;  Indels 0
          1 CCTTGAGGGTATTCCCTCC 20
          30 CCTTGAGGGTATTCCCTCC 11

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RESULT 15
S-09-474-432B-45/C
Sequence 45, Application US/09474432B
Patent No. 6538640

GENERAL INFORMATION:

APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpecky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Szwedler, David
APPLICANT: Zinner, Shawn

TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MBHB00-831-B (247/276)

CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19

PRIOR APPLICATION NUMBER: US 60/064, 866
PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: US 60/084, 727

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OM nucleic - nucleic search, using sw mode!

Run on: December 28, 2004, 10:09:11 ; Search time 3939 Seconds (without alignments)

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Sequence: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

Database : Published Applications_NA:
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 2: /cgn2_6_ptodata/2_pubnra/US07_PUBCOMB.seq: *
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 9: /cgn2_6_ptodata/2_pubnra/US08_PUBCOMB.seq: *
 10: /cgn2_6_ptodata/2_pubnra/US08_PUBCOMB.seq: *
 11: /cgn2_6_ptodata/2_pubnra/US09_PUBCOMB.seq: *
 12: /cgn2_6_ptodata/2_pubnra/US09_NEW_PUB_seq: *
 13: /cgn2_6_ptodata/2_pubnra/US10_PUBCOMB.seq: *
 14: /cgn2_6_ptodata/2_pubnra/US10_PUBCOMB.seq: *
 15: /cgn2_6_ptodata/2_pubnra/US10C_PUBCOMB.seq: *
 16: /cgn2_6_ptodata/2_pubnra/US10C_PUBCOMB.seq: *
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 19: /cgn2_6_ptodata/2_pubnra/US11_NEW_PUB_seq: *
 20: /cgn2_6_ptodata/2_pubnra/US11_NEW_PUB_seq: *
 21: /cgn2_6_ptodata/2_pubnra/US12_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	9 US-09-832-841-1	Sequence 1, Appli
2	20	100.0	20	10 US-09-937-839-1	Sequence 1, Appli
3	20	100.0	20	16 US-10-466-239-1	Sequence 1, Appli
4	20	100.0	20	17 US-10-618-162A-14	Sequence 1, Appli
5	20	100.0	20	17 US-10-618-162A-14	Sequence 1, Appli
c 6	20	100.0	20	17 US-10-783-635-1	Sequence 1, Appli
7	20	100.0	20	17 US-10-366-718-1	Sequence 1, Appli
8	20	100.0	20	17 US-10-468-717-1	Sequence 1, Appli
9	20	100.0	20	18 US-10-824-757-1	Sequence 1, Appli
10	20	100.0	20	18 US-10-234-041-9	Sequence 9, Appli
11	20	100.0	1032	15 US-10-424-599-51726	Sequence 51726, A
12	18	90.0	554	16	

RESULT 1
 US-09-832-841-1

Sequence 1, Application US/09832841
 Patent No. US20030098162A1
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, RYUICHI
 APPLICANT: OGIMARA, TOSHIKO
 APPLICANT: SUGIMOTO, KAZUHIKO
 APPLICANT: MAEDA, KAZUHIKO
 APPLICANT: KAWAMURA, IKUIC
 APPLICANT: CHIBA, TOSHIYUKI
 TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
 FILE REFERENCE: 18993-0PC

CURRENT APPLICATION NUMBER: US/09/832, 841
 CURRENT FILING DATE: 2001-04-12
 PRIORITY INFORMATION: Description of Artificial Sequence: Synthetic DNA
 PRIORITY APPLICATION NUMBER: 08/945, 805
 PRIORITY FILING DATE: 1998-01-06
 PRIORITY APPLICATION NUMBER: PCT/JP96/01234
 PRIORITY FILING DATE: 1996-05-10

NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence
 US-09-832-841-1

Query Match Score 100.0%; DB 9; Length 20;
 Best Local Similarity 100.0%; Pre. No. 2.6;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTGCC 20

ALIGNMENTS

Db 1 CCTTGAAAGGGATTCCCTCC 20

RESULT 2

US-09-937-839-1

; Sequence 1, Application US/09937839
; Publication No. US20030013195A1

; GENERAL INFORMATION:

; APPLICANT: Kaneda, Yasufumi
; TITLE OF INVENTION: Virus Envelope Vector for Gene Transfer

; CURRENT APPLICATION NUMBER: US/09/937,839

; FILE REFERENCE: 59150-8010

; CURRENT FILING DATE: 2002-02-21

; PCT/US APPLICATION NUMBER: PCT/JP01/00782

; PRIOR FILING DATE: 2001-02-02

; PCT/JP APPLICATION NUMBER: PCT/JP02/00865

; PRIOR FILING DATE: 2002-02-01

; PCT/JP APPLICATION NUMBER: PCT/JP02/00865

; PRIOR FILING DATE: 2002-02-02

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FasleQ for Windows Version 4.0

; SEQ ID NO: 1

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide

US-09-937-839-1

Query Match 100.0%; Score 20; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservatve 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 CCTTGAAAGGGATTCCCTCC 20

Qy 1 CCTTGAAAGGGATTCCCTCC 20

Db 1 CCTTGAAAGGGATTCCCTCC 20

Qy 1 CCTTGAAAGGGATTCCCTCC 20

Db 1 CCTTGAAAGGGATTCCCTCC 20

RESULT 4

US-10-466-239-1

; Sequence 1, Application US/10466239
; Publication No. US20040072726A1

; GENERAL INFORMATION:

; APPLICANT: Motohumi Morishita
; APPLICANT: Motohumi Aoki

; TITLE OF INVENTION: Decoy-containing pharmaceutical compositions and method of using

; CURRENT APPLICATION NUMBER: US/10/466,239

; CURRENT FILING DATE: 2003-07-10

; PCT/JP APPLICATION NUMBER: PCT/JP02/00865

; PRIOR FILING DATE: 2002-02-01

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 1

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: NF-?B decoy

; PUBLIC INFORMATION:

US-10-466-239-1

Query Match 100.0%; Score 20; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservatve 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 CCTTGAAAGGGATTCCCTCC 20

Qy 1 CCTTGAAAGGGATTCCCTCC 20

Db 1 CCTTGAAAGGGATTCCCTCC 20

Query Match 100.0%; Score 20; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservatve 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 CCTTGAAAGGGATTCCCTCC 20

Qy 1 CCTTGAAAGGGATTCCCTCC 20

Db 1 CCTTGAAAGGGATTCCCTCC 20

Query Match 100.0%; Score 20; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservatve 0; Mismatches 0;

Indels 0; Gaps 0;

Db 1 CCTTGAAAGGGATTCCCTCC 20

Qy 1 CCTTGAAAGGGATTCCCTCC 20

Db 1 CCTTGAAAGGGATTCCCTCC 20

RESULT 6

US-10-618-362A-14/c

Sequence 14, Application US/10618362A
 Publication No. US20040109843A1
 GENERAL INFORMATION:
 APPLICANT: Ryuichi Morishita
 APPLICANT: Motokuni Aoki
 APPLICANT: Toshio Ogihara
 APPLICANT: Tomio Kawasaki
 APPLICANT: Hiroyuki Makino
 TITLE OF INVENTION: Pharmaceutical composition containing decoy and use of the same
 FILE REFERENCE: ANGES-1 CIP US
 CURRENT APPLICATION NUMBER: US/10/618,362A
 CURRENT FILING DATE: 2003-07-10
 PRIOR APPLICATION NUMBER: PCT/JP02/00865
 PRIOR FILING DATE: 2002-02-01
 NUMBER OF SEQ ID NOS: 19
 SEQ ID NO: 14
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: NF-kappaB Decoy
 US-10-618-362A-14

Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 20 CCTTGAGGGATTCCCTCC 1

RESULT 7
 US-10-783-635-1
 Sequence 1, Application US/10783635
 Publication No. US20040142391A1
 GENERAL INFORMATION:
 APPLICANT: The Trustees of Columbia University in The City of New York
 APPLICANT: Schmidt, David M
 APPLICANT: Stern, David M
 APPLICANT: Schmidt, Ann Marie
 TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING
 TITLE OF INVENTION: INTERACTION OF A PEPTIDE WITH RAGE
 FILE REFERENCE: 56613
 CURRENT APPLICATION NUMBER: US/10/783,635
 CURRENT FILING DATE: 2004-02-20
 PRIOR APPLICATION NUMBER: US/09/1166,649
 PRIOR FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1

LENGTH: 20
 TYPE: DNA
 ORGANISM: human
 FEATURE:
 NAME/KEY: Primer
 LOCATION: (1)..(20)
 OTHER INFORMATION: Primer Against Human NF-kB
 NAME/KEY: Primer
 LOCATION: (1)..(20)
 OTHER INFORMATION: PCR Primer Against Human NF-kB
 US-10-783-635-1

Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 20 CCTTGAGGGATTCCCTCC 20

RESULT 8
 US-10-366-718-1
 Sequence 1, Application US/10366718
 Publication No. US20040162250A1
 GENERAL INFORMATION:
 APPLICANT: MORISHITA, RYUICHI
 APPLICANT: OGAWARA, TOSHI
 APPLICANT: SUGIMOTO, TOSHIK
 APPLICANT: MABEA, KAZUHIRO
 APPLICANT: KAWAMURA, IKU
 APPLICANT: CHIBA, TOSHIYUKI
 TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-kB
 FILE REFERENCE: 18933-0PCT
 CURRENT APPLICATION NUMBER: US/10/366,718
 CURRENT FILING DATE: 2003-02-14
 PRIORITY NUMBER: US/09/832,841
 PRIOR FILING DATE: 2001-04-12
 PRIORITY NUMBER: 08/945,805
 PRIOR FILING DATE: 1998-01-06
 PRIORITY NUMBER: PCT/JP96/01234
 PRIOR FILING DATE: 1996-05-10
 SOFTWARE: PatentIn Ver. 2.0
 NUMBER OF SEQ ID NOS: 4
 SEQ ID NO: 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 US-10-366-718-1

Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 9
 US-10-468-717-1
 Sequence 1, Application US/10468717
 Publication No. US20040162251A1
 GENERAL INFORMATION:
 APPLICANT: Ryulichi Morishita
 APPLICANT: Motokuni Aoki
 APPLICANT: Toshio Ogihara
 APPLICANT: Yasufumi Kanemura
 APPLICANT: Hiroshige Nakamura
 TITLE OF INVENTION: Pharmaceutical composition containing decoy and method of using t
 FILE REFERENCE: ANGES-2 US
 CURRENT APPLICATION NUMBER: US/10/468,717
 CURRENT FILING DATE: 2003-08-20
 PRIORITY NUMBER: PCT/JP02/00990
 PRIOR FILING DATE: 2002-02-06
 PRIORITY NUMBER: 2001-44350
 PRIOR FILING DATE: 2001-02-20
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 2.1
 SEQ ID NO: 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: NF-kappaB Decoy
 US-10-468-717-1

Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

Qy 1 CCTTGAGGGATTCCCTCC 20 ; LENGTH: 1032
 Db 1 CCTTGAGGGATTCCCTCC 20 ; TYPE: DNA ; ORGANISM: Homo Sapien
 ; US-10-234-041-9

RESULT 10
 US-10-824-757-1
 ; Sequence 1, Application US/10824757
 ; Publication No. US20040219674A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaneda, Yasufumi
 ; TITLE OF INVENTION: Virus Envelope Vector for Gene Transfer
 ; FILE REFERENCE: 59150-8010
 ; CURRENT APPLICATION NUMBER: US/10/824,757
 ; CURRENT FILING DATE: 2004-04-14
 ; PRIORITY NUMBER: US/09/937,839
 ; PRIOR APPLICATION NUMBER: 2002-02-21
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIORITY NUMBER: PCT/JP01/00782
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIORITY NUMBER: JP 2000-25596
 ; PRIOR FILING DATE: 2000-02-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic oligonucleotide
 US-10-824-757-1
 Query Match 100.0%; Score 20; DB 18; Length 20;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Missmatches 0;
 Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1 CCTTGAGGGATTCCCTCC 20

RESULT 11
 US-10-234-041-9
 ; Sequence 9, Application US/10234041
 ; Publication No. US003015371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Hession, Catherine A.
 ; APPLICANT: Lobb, Roy R.
 ; APPLICANT: Goetz, Susan E.
 ; APPLICANT: Osborn, Laurelee
 ; APPLICANT: Benjamin, Christopher D.
 ; APPLICANT: Rosa, Margaret D.
 ; TITLE OF INVENTION: Endothelial Cell-Leukocyte Adhesion Molecules (BLAMs) and Molecules Involved in Leukocyte Adhesion (MILAs)
 ; TITLE OF INVENTION: Adhesion
 ; FILE REFERENCE: B1-2ACP2DN2CN
 ; CURRENT APPLICATION NUMBER: US/10/234,041
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIORITY NUMBER: 03/473,764
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/342,642
 ; PRIOR FILING DATE: 1994-11-21
 ; PRIOR APPLICATION NUMBER: 07/608,298
 ; PRIOR FILING DATE: 1990-10-31
 ; PRIOR APPLICATION NUMBER: 07/452,675
 ; PRIOR FILING DATE: 1989-12-18
 ; PRIOR APPLICATION NUMBER: 07/359,516
 ; PRIOR FILING DATE: 1989-06-01
 ; PRIOR APPLICATION NUMBER: 07/345,151
 ; PRIOR FILING DATE: 1989-04-28
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 9

Qy 1 CCTTGAGGGATTCCCTCC 20 ; LENGTH: 1032
 Db 1 CCTTGAGGGATTCCCTCC 20 ; Score 20; DB 15; Length 1032;
 ; Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 20; Conservative 0; Missmatches 0;

RESULT 12
 US-10-424-599-51726
 ; Sequence 51726, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21 (53223) B
 ; CURRENT APPLICATION NUMBER: US/10/4244,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO: 51726
 ; LENGTH: 554
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_17722C.1
 US-10-424-599-51726
 Query Match 90.0%; Score 18; DB 16; Length 554;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Missmatches 0;

Qy 1 CCTTGAGGGATTCCCTCC 18
 Db 421 CCTTGAGGGATTCCCTCC 438

RESULT 13
 US-10-343-650A-97/C
 ; Sequence 97, Application US/10343650A
 ; Publication No. US20040067459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haga, Tatsuya
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-18-6347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 97
 ; LENGTH: 708
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(708)
 ; US-10-343-650A-97

Query Match Similarity 85.0%; Score 17; DB 16; Length 708;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

RESULT 14
 US-08-825-805-1548/c
 Sequence 1548, Application US/09825805
 Publication No. US20030004122A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 FILE REFERENCE: MBHB0-95-J (400/032)
 CURRENT FILING DATE: 2001-07-25
 NUMBER OF SEQ ID NOS: 446
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 399
 LENGTH: 40
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molecule
 US-09-916-466-399
 Query Match 84.0%; Score 16.8; DB 10; Length 40;
 Best Local Similarity 90.0%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGATTCCTCC 20
 Db 24 CCTTGAGGAGTTCTCC 5
 Search completed: December 28, 2004, 13:15:13
 Job time : 3940 secs

RESULT 15
 US-09-916-466-399/c
 Sequence 399, Application US/09916466
 Publication No. US2003006495A1
 GENERAL INFORMATION:
 APPLICANT: Akhtar, Saghif
 FILE REFERENCE: MBHB0-95-J (400/032)
 CURRENT FILING DATE: 2001-07-25
 NUMBER OF SEQ ID NOS: 446
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 399
 LENGTH: 40
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molecule
 US-09-916-466-399
 Query Match 84.0%; Score 16.8; DB 10; Length 32;
 Best Local Similarity 90.0%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CCTTGAGGATTCCTCC 20
 Db 20 CCTTGAGGAGTTCTCC 1

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Result No.	Score	Query Match	Length	DB ID	Description
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3	20	100.0	768	9	CR139070 CR139070
4	18	90.0	504	7	CO695591 CO695591
5	18	90.0	604	8	CC133636 CC133636
6	18	90.0	627	5	BW242276 BW242276
7	17.4	87.0	269	2	BB002216 BB002216
8	17.4	87.0	453	6	CA857737 CA857737
9	17.4	87.0	478	4	BJ072801 BJ072801
10	17.4	87.0	529	5	BX844476 BX844476
11	17.4	87.0	580	4	BM179747 BM179747
12	17.4	87.0	606	7	CR585617 CR585617
13	17.4	87.0	671	5	BX850643 BX850643
14	17.4	87.0	885	6	CD303290 CD303290
15	17.4	87.0	938	8	CC091597 CC091597
16	17.4	87.0	1146	4	BG531353 BG531353
17	17.4	87.0	1172	8	CC239703 CC239703
18	17.4	87.0	1172	8	CC302285 CC302285
19	17	85.0	350	17	R25866 R25866
20	17	85.0	512	2	BB755468 BB755468
21	17	85.0	831	4	BB1870073 BB1870073
22	16.8	84.0	152	2	BB061146 BB061146
23	16.8	84.0	202	9	CG632344 CG632344
24	16.8	84.0	246	2	AW571808 AW571808

Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-513-9222
 Fax: 81-45-513-9216
 Email: genome-reseq@riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watabiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of cap-trapper-selected cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing Pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 A cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.jp/>) for
 further details.

FEATURES
source

1. .334 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="L930275P17"
 /tissue_type="whole body"
 /dev_stage="17.5 days embryo"
 /clone.lib="RIKEN full-length enriched, 17.5 days embryo
 whole body"

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 334;
 Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Gaps 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1.99 CCTTGAGGGATTCCCTCC 218

BF385710 602047366F1 NCI_CGAP_Li9 701 bp mRNA linear EST 27-NOV-2000
 mRNA sequence.
 BF385710 EST.
 BF385710.1 GI:11367015

FEATURES
source

1 (bases 1 to 701)
 NIH-MGC URL: <http://mgc.ncbi.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LIAM9534 row: C column: 18

High quality sequence stop: 639.

Location/Qualifiers

1..701

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone=IMAGE:4196681"

/lab_host="DE10B (T1 phage-resistant)"

/clone.lib="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 701;

Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1.62 CCTTGAGGGATTCCCTCC 181

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="NHPPI3791"

/clone.lib="NHPPI"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="FVB/N"

/clone=IMAGE:4196681"

/lab_host="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 701;

Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 1.62 CCTTGAGGGATTCCCTCC 181

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="NHPPI3791"

/clone.lib="NHPPI"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="FVB/N"

/clone=IMAGE:4196681"

/lab_host="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 768;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 636 CCTTGAGGGATTCCCTCC 655

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="NHPPI3791"

/clone.lib="NHPPI"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 768;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 636 CCTTGAGGGATTCCCTCC 655

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="NHPPI3791"

/clone.lib="NHPPI"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 768;

Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAGGGATTCCCTCC 20
 Db 636 CCTTGAGGGATTCCCTCC 655

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone="NHPPI3791"

/clone.lib="NHPPI"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: NotI;

Site 2: Sall; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

KEYWORDS EST: *Canis familiaris* (dog)
ORGANISM SOURCE: *Canis familiaris*

REFERENCE AUTHOR: *Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis*.
1 (bases 1 to 504)
COMMENT: *Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H., Henrich, J. and Loebert, R.*
TITLE: *Dog arrayTAG cDNA clone collection*
JOURNAL: *Unpublished (2004)*
COMMENT: *Contact: Thomas Schlueter*
COMMENT: *LION bioscience AG*
COMMENT: *Waldhoferstrasse 98, D-69123 Heidelberg, Germany*
COMMENT: *Tel: +49 6221 4038 150*
COMMENT: *Fax: +49 6221 4038 290*
COMMENT: *Email: Thomas.Schlueter@lionbioscience.com.*

FEATURES Source
1. '504
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="D011-Kidney"
/note="Organ: Kidney; Vector: Dog pBluescript LION"

ORIGIN
Query Match 90.0%; Score 18; DB 7; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTGAACTGGATTCCCTCC 20
Db 440 TTGAACTGGATTCCCTCC 457

RESULT 5
LOCUS CC133636 604 bp DNA linear GSS 16-APR-2003
DEFINITION NDL_80H15_T7 Notre Dame Liverpool Aedes aegypti genomic clone
VERSION CC133636
KEYWORDS SOURCE
ORGANISM *Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Culicoidea; Aedes; Aedes aegypti; Aedes aegypti; Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Aedes; Stgomyia.*
COMMENT: *Loftus, B., Shetty, J., Knudson, D. and Severson, D.*
COMMENT: *BAC end sequencing of Aedes aegypti*
COMMENT: *Unpublished (2003)*
COMMENT: *Other GSSs: NDL_80H15_SP6*
COMMENT: *Contact: Brendan Loftus*
COMMENT: *Department of Eukaryotic Genomics*
COMMENT: *TIGR*
COMMENT: *9712 Medical Center Drive, Rockville, MD 20850, USA*
COMMENT: *tel: 301-838-3543*
COMMENT: *Fax: 301-838-0208*
COMMENT: *Email: enta@tigr.org*
COMMENT: *Library was provided by David Severson*
COMMENT: *Seq. Primer: T7*
COMMENT: *Class: BAC ends.*

FEATURES Source
1. '604
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL_80H15"

RESULT 6
LOCUS BW242276/c
DEFINITION BW242276 Nori Satoh unpublished cDNA library, tailbud embryo *Ciona intestinalis* cDNA clone citb101n15', mRNA sequence.
VERSION BW242276.1
KEYWORDS EST.
SOURCE
ORGANISM *Ciona intestinalis*
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiaceae; Enterogona;
Phlebobranchia; Cionidae; Ciona.
COMMENT: *1 (bases 1 to 627)*
COMMENT: *Satoh, Y., Shin-i, T., Kohara, Y. and Satoh, N.*
COMMENT: *Expressed genes in *Ciona intestinalis* (2002c)*
COMMENT: *Unpublished (2002)*
COMMENT: *Contact: Nori Satoh*
COMMENT: *Department of Zoology*
COMMENT: *Kyoto University*
COMMENT: *Sakyo-ku, Kyoto, Kyoto 606-8502, Japan*
COMMENT: *Tel: 81-75-753-1081*
COMMENT: *Fax: 81-75-705-1113*
COMMENT: *Email: satoh@ascidian.zool.kyoto-u.ac.jp.*

FEATURES Source
1. '627
/organism="Cliona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb101n15"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"
/note="Nori Satoh unpublished cDNA library, tailbud embryo"

ORIGIN
Query Match 90.0%; Score 18; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 4.1.e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTGAACTGGATTCCCTCC 19
Db 451 CTTGAACTGGATTCCCTCC 434

RESULT 7
LOCUS BB002216
DEFINITION BB002216 RIKEN full-length enriched, 0 day neonatal skin *Mus musculus* cDNA clone 463143cK12_3, similar to DB0005 Human mRNA for KIAA0183 gene, mRNA sequence.
VERSION BB002216.1
KEYWORDS EST.
SOURCE
ORGANISM *Mus musculus* (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RESULT 9	
BJ072801/c	EST
LOCUS	BJ072801
DEFINITION	NIBB Mochii normalized Xenopus tail bud library Xenopus laevis cDNA clone XLO99p175 , mRNA sequence.
ACCESSION	BJ072801
VERSION	BA072801.1
KEYWORDS	EST.
SOURCE	GI:17502990
ORGANISM	Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.	
1 (basses 1 to 478)	
Kitayama,A., Terasaki,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.	
TITLE	Expressed genes in X. laevis embryo
JOURNAL	Unpublished (2001)
COMMENT	Contact: Tadatsugu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856

```

x: 81-559-81-6855
mail: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL:
http://xenopus.nibb.ac.jp/
Location/Qualifiers
1. 478
  organism="Xenopus laevis"
  /mol_type="mRNA"
  /db_xref="taxon:8355"
  /clone="XL099p17"
  /tissue="whole embryo"
  /dev_stage="stage 25"
  /clone_id="NIBB Mochii normalized Xenopus tail bud
  1a"

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ORIGIN	library	Query	Match	87.0*	Score	17.4;	DB	4;	Length	478;
		Best	Local	Similarity	94.7*	Pred.	No.	7.9e+02;		
		Matches	18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps
Qy		2	CTTGAGGGGATTTCCTCC	20						
Ddb		336	CTTGAGGGGATTTCCTCC	318						

RESULT 10
 BX44476/C LOCUS BX844476 LOCUS DEFINITION BX844476 NICHD XGC Emb1 529 bp mRNA linear laevis cDNA clone IMAGP98B114205
 ACCESSION BX844476
 VERSION BX844476.1
 KEYWORDS EST
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 RELEVANT RECORDS
 COMMENTS

REFERENCE AUTHORS TITLE JOURNAL COMMENT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodidae; Xenopus; Xenopus.
 Xenopodidae; Xenopus; Xenopus.
 1 (bases 1 to 529)
 Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
 Schroth, A., Korn, B., and Landgrebe, J.
 Xenopus laevis Unigene Set 1 (RZPDLIB No. 988)
 Unpublished (2003)
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: INAGP998B1814205.
 REFERENCE AUTHORS TITLE JOURNAL COMMENT
 1 (bases 1 to 529)
 Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
 Schroth, A., Korn, B., and Landgrebe, J.
 Xenopus laevis Unigene Set 1 (RZPDLIB No. 988)
 Unpublished (2003)
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: INAGP998B1814205.

FEATURES	Source
<p>No. 998 http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus laevis UniGene Set 1 (RZPDLIB No. 988) http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=988 Context: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heinbergsweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de</p> <p>This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: SP6, 5' ATTTGGTGCACATAG 3'.</p> <p>Location/Qualifiers</p> <p>1. -529</p> <p>/organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="IMAGE9981814205"; IMAGE:6633714" /tissue="embryo (stage 10)" /lab_host="DH10B (phage-resistant)" /clone_lib="NICHID XGC Emb1" /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."</p>	

ORIGIN	FEATURES	Source	VERSION	KEYWORDS	SOURCE	ORGANISM	COMMENT
/clone_lib="NICHID XGC_Emb4" /note="Organ: whole embryo; Vector: PCMV-SPORT6; Site: 1; Note: Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."	Query Match Best Local Similarity 87.0%; Score 17.4; DB 4; Length 580; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 2 CTTGAAGGATTCCCTCC 20 Db 346 CTTGAAGGATGCCCTCC 328		BX850643.1	GI:39739085 EST. Xenopus laevis (African clawed frog)			
RESULT 12 CR585617/c LOCUS CR585617 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA052j02 DEFINITION 3', mRNA sequence.			CR585617/c LOCUS CR585617 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA052j02 DEFINITION 3', mRNA sequence.		606 bp	mRNA linear	EST 26-JUL-2004
ACCESSION CR585617 VERSION CR585617.1 KEYWORDS EST. ORGANISM Xenopus tropicalis (western clawed frog) SOURCE Xenopus tropicalis Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Silurana.							
REFERENCE AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. TITLE Unpublished (2004) JOURNAL Contact: Croning MDR COMMENT Hinxton, Cambridge, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST Project 2001 TOPICAL SEQUENCE ID: THdA052j02.q1k17 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett. Seq primer: T7							
ORIGIN	Query Match Best Local Similarity 94.7%; Score 17.4; DB 5; Length 671; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		BX850643.1	GI:39739085 EST. Xenopus laevis (African clawed frog)			
/clone_lib="NICHID XGC_Emb4" /note="Organ: whole embryo; Vector: PCMV-SPORT6; Site: 1; Note: Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."							
RESULT 14 CD303290/c LOCUS AGENCOURT 14233231 NICHID_XGC_Brn1 mRNA cDNA clone DEFINITION IMAGE:6955295', mRNA sequence.			CD303290	885 bp	mRNA	linear	EST 27-MAY-2003
ACCESSION CD303290 VERSION CD303290.1 KEYWORDS EST. ORGANISM Xenopus laevis SOURCE Xenopus laevis COMMENT Xenopodinae; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus.							
REFERENCE 1 (bases 1 to 885) AUTHORS NIH-MCG http://mgc.nci.nih.gov/ TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniel S. Gerhard, Ph.D. JOURNAL Office of Cancer Genomics							
ORIGIN	Query Match Best Local Similarity 94.7%; Score 17.4; DB 7; Length 606; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		BX850643	GI:39739085 EST. Xenopus laevis (African clawed frog)			
/clone_lib="NICHID XGC_Emb4" /note="Organ: whole embryo; Vector: PCMV-SPORT6; Site: 1; Note: Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."							
RESULT 13 BX850643/c LOCUS BX850643 NICHID XGC_Emb4 671 bp mRNA linear DEFINITION BX850643 NICHID XGC_Emb4 Xenopus laevis cDNA clone IMAGp998H1310927 /IMAGE:4959036 5', mRNA sequence. ACCESSION BX850643							

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov

Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>

Plate: LLAM4581 Row: C column: 16
High quality sequence stop: 687.

FEATURES
Source
1. 885
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:695529"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHID XGC_Brnl"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dR.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN
Query Match 87.0%; Score 17.4; DB 6; Length 885;
Best Local Similarity 94.7%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTTGAGGGATTCCTTC 20
Db 337 CTTGAGGGATTCCTTC 319

RESULT 15
CC091597
LOCUS CCG091597 938 bp DNA linear GSS 16-APR-2003
DEFINITION CSU-K33r-24N21-T7 CSU-K33r Aedes aegypti genomic clone
ACCESSION CSU-K33r-24N21, genomic survey sequence.
VERSION CC091597
KEYWORDS CC091597.1 GI:29950049
GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryot; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.
1 (bases 1 to 938)
AUTHORS Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
TITLE End sequencing of Aedes aegypti BACs
JOURNAL Unpublished (2003)
COMMENT Other GSes: CSU-K33r-24N21-SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: entaa@igr.org

Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.
Seq primer: T7
Class: BAC ends
Source
1. 938
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Rockville"
/db_xref="taxon:7159"
/clone="CSU-K33r-24N21"

FEATURES
Source
1. 846
/CCTTGAGGGATTCCTTC 19
Db

ORIGIN
Query Match 87.0%; Score 17.4; DB 8; Length 938;
Best Local Similarity 94.7%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCTTGAGGGATTCCTTC 19
Db 846 CCTTGAAAGGATTTCCTTC 864

Search completed: December 28, 2004, 10:09:04
Job time : 2936 secs

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